

Brief Report

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Brief Report

Transcriptome for Identification of Biomarkers for Diagnosis and Targeted Therapy of Type 1 Diabetes

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Abstract

A Transcriptome dataset of whole blood RNA-seq data from type 1 diabetic (T1D) patients and healthy volunteers was deposited on GEO dataset in 2020 (GSE123658). Because of recurrent citations to the transimmunom dataset, read counts at gene level are revised and putative up-regulated biomarkers for T1D diagnosis and targeted therapy are presented. We present TRHDE, GOLGA8I, HBZ, BOLA2B, SPATA22, SEMA6B and FOXQ1 genes as putative biomarkers for diagnosis ($\log_2FC \geq 1.5$ and $p \leq 0.05$). All together, our result points to GSE123658 dataset as source of biomarkers and therapy target genes.

Keywords: transcriptome; type 1 diabetes; biomarkers; target genes

Introduction

A Transcriptome dataset of whole blood RNA-seq data from type 1 diabetic (T1D) patients and healthy volunteers was deposited on GEO dataset in 2020 (GSE123658). Starting with a protocol for recruitment of participants followed by sample acquisition [1], whole blood RNA from 43 healthy donors and 39 T1D patients were sequenced and the corresponding gene expressions were estimated. Since the upload of the database, GSE123658 was used for in computational experiments in the identification of hub genes related to type 1 diabetes progression [2], and the discovery of gene signatures associated with T Cells and Natural Killer Cells [3]. Moreover, TSPO was identified as the only gene differentially expressed in both conditions T1D ($\log_2FC = 0.504$, $p = 0.0319$) and epilepsy ($\log_2FC = 0.562$, $p < 0.001$) [4]. Finally, three independent diabetes-related GEO datasets - including transimmunom - and found 117 common T1D genes [5]. Because of recurrent citations to the transimmunom dataset, read counts at gene level are revised and putative up-regulated biomarkers for T1D diagnosis and targeted therapy are presented.

Type 1 diabetes (T1D) is an autoimmune disease resultant from β -cell destruction in the pancreas destruction in the pancreas [6–8]. The molecular mechanisms underlying T1D are known to be related to antigen presentation [9,10], beta cell autoimmunity [11,12] immune tolerance [13,14], T cell response [15–17], chemokine production [18], among other [19–21]. Candidate genes for diagnostic biomarkers can be identified when their expression is high in patients compared to healthy controls. Meanwhile, treatment targets will be found among genes with high interactivity rather than high expression.

Methods

The reads of each sample were then aligned against the Human genome using default parameters of hisat2 for paired reads of forward-cell destruction in the pancreasstranded library. The genome index database was built over the Ensembl Human genome [22] version GRCh37. Next, featureCounts [23] parameters was also adjusted for analysis of paired reads of forward-cell destruction in the pancreasstranded library at gene level. The gene annotation used here was also obtained from Ensembl version GRCh37. The read counts for each sample was merged in a final table

and analyzed with R [25] scripts developed specifically for this dataset. Only protein coding genes located on autosomal chromosomes were further considered.

Results

Only seven up-regulated genes are found to be differently expressed (DE) between T1D and healthy samples when $\log_2FC \geq 1.5$ and $\text{padj} \leq 0.05$.

Table 1. Up-regulated biomarkers whose fold change ($\log_2FC$) are ≥ 1.5 and a $\text{padj} \leq 0.05$ between T1D and healthy samples.

Gene name	log2FC	pvalue	padj	healthy		T1D	
				mean	sd	mean	sd
TRHDE	1.66	1.29E-03	1.35E-02	0.96	1.38	2.97	7.19
GOLGA8I	1.77	8.25E-06	4.95E-04	1.20	1.15	4.26	9.54
HBZ	1.54	1.09E-03	1.21E-02	2.23	3.21	6.64	11.97
<u>BOLA2B</u>	1.95	8.05E-05	2.06E-03	4.67	9.35	17.43	39.83
SPATA22	1.89	3.56E-04	5.58E-03	1.35	2.12	4.60	9.90
SEMA6B	1.65	3.74E-08	1.52E-05	9.73	6.02	29.94	45.24
FOXQ1	2.53	1.97E-05	8.29E-04	1.01	1.89	5.88	17.54

Conclusions

Up-regulated genes whose fold change ($\log_2FC$) are ≥ 1.5 and a $\text{padj} \leq 0.05$ between T1D and healthy samples are good candidate for diagnosis biomarkers. Additional molecules can also be found among the down-regulated genes. Furthermore, genes for therapy can be mined by applying criteris to filter out biomarkers with high interactome conectivity.

Declarations: Felipe Leal Valentim FLV submitted the dataset to the GEO database in 2020 (GSE2020123658). FLV was with Unit  Immunologie-Immunopathologie-Immunoth rapie, INSERM/UPMC for the submission of the dataset. FLV is currently with the Department of Mechatronics and Mechanical Systems Engineering of the Polytechnic School of the University of S o Paulo. Scripts to analyse the read counts are found in the github depository : <https://github.com/datasciencebioinformatics/TranscriptomeFingerprintAnalysis>.

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